

22. An isolated polynucleotide encoding a polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence of SEQ ID NO:1,

b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1,

D, c) a biologically active fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1, and

d) an immunogenic fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1.

23. An isolated polynucleotide encoding a polypeptide of SEQ ID NO:1.

24. An isolated polynucleotide of claim 23 comprising the sequence of SEQ ID NO:2.

25. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 22.

26. A cell transformed with a recombinant polynucleotide of claim 25.

27. A method for producing a polypeptide encoded by a polynucleotide of claim 22, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide of claim 22, and

b) recovering the polypeptide so expressed.

28. An isolated polynucleotide selected from the group consisting of:
- a) a polynucleotide comprising a polynucleotide sequence of SEQ ID NO:2,
 - b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence of SEQ ID NO:2,
 - c) a polynucleotide complementary to the polynucleotide of a),
 - d) a polynucleotide complementary to the polynucleotide of b), and
 - e) an RNA equivalent of a)-d).

29. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 28.

30. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 28, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

31. A method of claim 30, wherein the probe comprises at least 60 contiguous nucleotides.

32. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 28, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

33. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 24, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

34. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 28 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 28 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.